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Gencore version 4.5

OM protein - protein search, using sw model
Run on: July 3, 2002, 10:30:26 ; Search time 25.2 Seconds
(without alignments)
34.318 Million cell updates/sec

Title: 09-403627-1

Perfect score: 45

Sequence: 1 avdlshflk 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 788

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR71;*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	17	37.8	9 2	S07205
2	17	37.8	9 2	S07204
3	16	35.6	9 2	S07241
4	16	35.6	9 2	D48186
5	15	33.3	8 2	PC4131
6	15	33.3	9 2	JN0026
7	14	31.1	5 4	A58728
8	14	31.1	7 2	S20446
9	14	31.1	7 2	S78034
10	14	31.1	8 2	R42057
11	14	31.1	8 2	S66296
12	14	31.1	9 2	B39841
13	14	31.1	9 2	A39841
14	31.1	9 2	C57444	
15	13	28.9	6 2	A46474
16	13	28.9	7 2	S08606
17	13	28.9	7 2	S4207
18	13	28.9	7 2	PT0520
19	13	28.9	9 2	PT0238
20	12	26.7	4 2	I38889
21	12	26.7	4 2	A35779
22	12	26.7	4 2	PT0712
23	12	26.7	5 2	S70154
24	12	26.7	7 2	PC2370
25	12	26.7	7 2	PN0649
26	12	26.7	7 2	S29735
27	12	26.7	8 2	XGHUEU
28	12	26.7	8 2	T14905
29	12	26.7	8 2	B27867

RESULT 1
S07205
litorin 2-Glu - Australian tree frog (Litoria aurea)
C;Species: Litoria aurea
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07205
R;Anastasi, A.; Montecuccchi, P.; Angelucci, F.; Ersamer, V.; Endean, R.
Experientia 33, 1289, 1977
A;Title: Glu(Ome)(2)-litorin, the second bombesin-like peptide occurring in methanol
A;Reference number: S07205; MUID:78003546
A;Accession: S07205
A;Molecule type: protein
A;Residues: 1-9 <ANAL>
C;Superfamily: gasrin-releasing peptide
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: amidated carboxyl end (Met) #status experimental
F;9/Modified site: amidated carboxyl end (Met) #status experimental

ALIGNMENTS

QY	4 lshfl 8	OY	4 lshfl 8	Db	5 VGHFM 9
litorin 2-Glu - Au	litorin I - Australian tree frog (Litoria aurea)				
litorin I	litorin I - Australian tree frog (Litoria aurea)				
Ritoin - Rhode's					
ATPase RL subunit					
hypothetical prote					
sperm-activating p					
serrewettin W2 - S					
elastase - Pseudom					
ribosomal protein					
fibroblast growth					
Na+-transporting A					
dex-transcarase (EC					
3.1.1.9					
sucrose 3'-glucosyl					
neuropeptide Grb-A					
Fc epsilon RIB -					
hypothetical prote					
gramicidin S synth					
T-cell receptor be					
alpha-dextrin endo					
polyphosphopeptide-glu					
urine glycoprotein					
hypothetical prote					
homeotic protein U					

callifuramide 8 -
T-cell receptor ga

hypothetical prote

{Phe-61}-mocat - s

Ig heavy chain v

pep-tachykinin - p

neuropeptide Antho

peptidyl-dipeptida

botin B - Citroba

pep fimbrial regul

dnna protein - pse

californamide 11

DNA topoisomerase

sperm-activating p

sperm-activating p

locustamycininhibit

RESULT 2
S07204
litorin I - Australian tree frog (Litoria aurea)
C;Species: Litoria aurea
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07204
R;Anastasi, A.; Espamer, V.; Endean, R.
Experientia 31, 510-511, 1975
A;Title: Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide
A;Reference number: S07204; MUID:75187011
A;Accession: S07204
A;Molecule type: protein
A;Residues: 1-9 <ANAL>
C;Superfamily: gastrin-releasing peptide
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: Pyrrolidine carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Met) #status experimental

QY	4 lshfl 8	QY	4 lshfl 8
litorin 2-Glu - Au	litorin I - Australian tree frog (Litoria aurea)		
litorin I	litorin I - Australian tree frog (Litoria aurea)		
Ritoin - Rhode's			
ATPase RL subunit			
hypothetical prote			
sperm-activating p			
serrewettin W2 - S			
elastase - Pseudom			
ribosomal protein			
fibroblast growth			
Na+-transporting A			
dex-transcarase (EC			
3.1.1.9			
sucrose 3'-glucosyl			
neuropeptide Grb-A			
Fc epsilon RIB -			
hypothetical prote			
gramicidin S synth			
T-cell receptor be			
alpha-dextrin endo			
polyphosphopeptide-glu			
urine glycoprotein			
hypothetical prote			
homeotic protein U			

Db : |||
 5 WGFM 9

A;Residues: 1-8 <KAW>
 A;Cross-references: DDBJ:d50473; NTDB:91217594
 A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0

RESULT 3
 S07241 |litorin - Roehde's leaf frog
 C;Species: Phyllomedusa rohdei (Roehde's leaf frog)
 C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
 C;Accession: S07241
 R;Barra, D.; Falconieri Ersbamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Ersbamer,
 FEBS Lett. 182, 53-56, 1985
 A;Title: Roehde-litorin: a new peptide from the skin of Phyllomedusa rohdei.
 A;Reference number: S07241; MUID:85127560
 A;Molecule type: protein
 A;Accession: S07241
 A;Residues: 1-9 <BAR>
 A;Molecule type: protein
 C;Superfamily: gastrin-releasing peptide
 C;Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.6%; Score 16; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+0; 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 hf1 8
 |||:
 Db 7 HFM 9

RESULT 4
 D48186 ATPase R1 subunit - wood tobacco (fragment)
 C;Species: Nicotiana syvestris (wood tobacco)
 C;Accession: D48186
 R;De Paep, R.; Forchion, A.; Chetrit, P.; Vodel, F.
 Proc. Natl. Acad. Sci. U.S.A. 90, 5935-5938, 1993
 A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase
 A;Reference number: A48186; MUID:93317598
 A;Accession: D48186
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <DEI>
 A;Experimental source: pollen
 A;Note: sequence extracted from NCBI backbone (NCBIP:134871)

Query Match 35.6%; Score 16; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05; 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 vdlsfh 7
 |||:
 Db 3 VDLAPY 8

RESULT 5
 PC4131 hypothetical protein B [imported] - Pseudomonas aeruginosa (fragment)
 C;Species: Pseudomonas aeruginosa
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C;Accession: PC4131
 R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
 Gene 167, 87-91, 1995
 A;Title: Sequencing and characterization of the downstream region of the genes encoding
 Y for biosynthesis of heme d1.
 A;Reference number: JC4552; MUID:96144254
 A;Accession: PC4131
 A;Status: Preliminary
 A;Molecule type: DNA

RESULT 6
 JN0026 sperm-activating peptide SAP-b - sea urchin (*Clypeaster japonicus*)
 N;Alternate names: [His-6]-mosact
 C;Species: Clypeaster japonicus
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Aug-2000
 C;Accession: JN0026; Be0973
 R;Suzuki, N.; Kurita, M.; Yoshino, K.I.; Kajura, H.; Nomura, K.; Yamaguchi, M.
 Zool. Sci. 4, 649-656, 1987
 A;Title: Purification and structure of mosact and its derivatives from the egg jelly
 A;Reference number: JN0026
 A;Accession: JN0026
 A;Molecule type: protein
 A;Residues: 1-9 <SUZ>
 R;Takao, T.; Yoshino, K.; Suzuki, N.; Shimomishi, Y.
 Biomed. Environ. Mass Spectrom. 19, 705-712, 1990
 A;Title: Analysis of post-translational modifications of proteins by accurate mass me
 A;Reference number: A60973; MUID:91167743
 A;Accession: Be0973
 A;Molecule type: protein
 A;Residues: 1-9 <TAK>
 C;Comment: Forms with and without the bromohistidine moiety were purified separately.
 C;Superfamily: unassigned animal peptides
 C;Keywords: bromine
 F;6/Modified site: bromohistidine (His) (partial) #status experimental

Query Match 33.3%; Score 15; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05; 0; Gaps 0;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 dlshf1 8
 |||:
 Db 3 DSAHLI 8

RESULT 7
 A58728 serranettin W2 - *Serratia marcescens*
 C;Species: Serratia marcescens
 C;Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
 C;Accession: A58728
 R;Matsuura, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
 J. Bacteriol. 174, 1769-1776, 1992
 A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent
 A;Reference number: A58728; MUID:92133260
 A;Accession: A58728
 A;Molecule type: polypeptide
 A;Residues: 1-5 <MAT>
 A;Experimental source: strain NS 25
 C;Comment: A surfactant lipopeptide promoting flagellum-independent surface transloca
 C;Keywords: blocked amino end; D-amino acid; lipoprotein; unenc
 F;1/Modified site: D-leucine (Leu) #status experimental
 F;4/Modified site: D-phenylalanine (Phe) #status experimental
 F;1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Ieu-Lle) #status e

A;Residues: 1-8 <KAW>
 A;Cross-references: DDBJ:d50473; NTDB:91217594
 A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0

Query Match 33.3%; Score 15; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.8e-05; 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 dlshf1 8
 |||:
 Db 3 DLRRRL 8

RESULT 7
 A58728 serranettin W2 - *Serratia marcescens*
 C;Species: Serratia marcescens
 C;Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
 C;Accession: A58728
 R;Matsuura, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
 J. Bacteriol. 174, 1769-1776, 1992
 A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent
 A;Reference number: A58728; MUID:92133260
 A;Accession: A58728
 A;Molecule type: polypeptide
 A;Residues: 1-5 <MAT>
 A;Experimental source: strain NS 25
 C;Comment: A surfactant lipopeptide promoting flagellum-independent surface transloca
 C;Keywords: blocked amino end; D-amino acid; lipoprotein; unenc
 F;1/Modified site: D-leucine (Leu) #status experimental
 F;4/Modified site: D-phenylalanine (Phe) #status experimental
 F;1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Ieu-Lle) #status e

Query Match 31.1%; Score 14; DB 4; Length 5;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 4 lshfl 8
 Db 1 LSTFI 5

RESULT 8
 S20446 elastase - Pseudomonas aeruginosa
 C;Species: Pseudomonas aeruginosa
 C;Accession: S20446
 C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
 R;Kessler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
 FEB Lett, 299, 291-293, 1992
 A;Title: Identification of cleavage sites involved in proteolytic processing of Pseudomonas aeruginosa
 A;Reference number: S20446; MUID:92183956
 A;Accession: S20446
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <KES>

Query Match 31.1%; Score 14; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 avd 4
 Db 1 AADL 4

RESULT 9
 S78024 ribosomal protein Yml21, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
 C;Species: Saccharomyces cerevisiae
 C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
 C;Accession: S78024
 R;Kirakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittmaier, J.; Bloch, 245, 449-456, 1997
 A;Title: Identification and characterization of the genes for mitochondrial ribosomal proteins
 A;Reference number: S78018; MUID:97296414
 A;Accession: S78024
 A;Molecule type: protein
 A;Residues: 1-7 <KIT>
 C;Genetics:
 A;Genome: nuclear
 C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 31.1%; Score 14; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 lshflk 9
 Db 2 LXNLK 7

RESULT 10
 A42057 fibroblast growth factor receptor 1, secreted - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
 C;Accession: A42057
 R;Merner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
 Mol. Cell. Biol. 12, 82-88, 1992
 A;Title: Differential splicing in the extracellular region of fibroblast growth factor receptor 1
 A;Reference number: A42057; MUID:92107200
 A;Accession: A42057
 A;Status: preliminary

Query Match 31.1%; Score 14; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 4 lshfl 8
 Db 3 LISFL 7

RESULT 11
 S66296 Na+-transporting ATP synthase (EC 3.6.1.-) chain c - Acetobacterium woodii (fragment)
 N;Alternate names: Atpase chain c
 C;Species: Acetobacterium woodii
 C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
 C;Accession: S66296
 R;Reidinger, J.; Mueller, V.; Eur. J. Biochem, 223, 275-283, 1994
 A;Title: Purification of ATP synthase from Acetobacterium woodii and identification a
 A;Reference number: S45648; MUID:94307271
 A;Accession: S66296
 A;Molecule type: protein
 A;Residues: 1-8 <REI>
 A;Experimental source: DSM 1030
 C;Keywords: hydrolase

Query Match 31.1%; Score 14; DB 2; Length 8;
 Best Local Similarity 28.6%; Pred. No. 2.8e+05;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 3 dishflk 9
 Db 2 EILDIFIK 8

RESULT 12
 B39841 dextrantranscruase (EC 2.4.1.5) - Streptococcus sobrinus (fragment)
 C;Species: Streptococcus sobrinus
 C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 23-Jun-1993
 C;Accession: B39841
 R;Mooser, G.; Hefta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
 J. Biol. Chem. 266, 8916-8922, 1991
 A;Title: Isolation and sequencing of an active-site peptide containing a catalytic aspartate residue from streptococcal dextrantranscruase
 A;Reference number: A39841; MUID:91224988
 A;Accession: B39841
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <MOO>
 C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 31.1%; Score 14; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 avd 3
 Db 7 AVD 9

RESULT 13
 A39841 sucrose 3'-glucosyltransferase (EC 2.4.1.-) - Streptococcus sobrinus (fragment)
 C;Species: Streptococcus sobrinus
 C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 21-Mar-1996

C;Accession: A39841
 R;Mooser, G.; Hefta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
 J. Biol. Chem. 266, 8916-8922, 1991
 A;Title: Isolation and sequence of an active-site peptide containing a catalytic aspartic acid residue.
 A;Accession: A39841; MUID:91224988
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: j-i-9 <RHO>
 C;Keywords: glycosyltransferase; hexosyltransferase

Search completed: July 3, 2002, 10:33:24
 Job time: 178 sec

Query Match 31.1%; Score 14; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 avd 3
 |||
 Db 7 AVD 9

RESULT 14
 C57444
 neuropeptide Grb-AST B3 - two-spotted cricket
 C;Species: Gryllus bimaculatus (two-spotted cricket)
 C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
 C;Accession: C57444
 R;Lorenz, M.W.; Keilner, R.; Hoffmann, K.H.
 J. Biol. Chem. 270, 21103-21108, 1995
 A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
 A;Reference number: A57444; MUID:95403341
 A;Accession: C57444
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <LOR>

Query Match 31.1%; Score 14; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 dls 5
 |||
 Db 4 DLS 6

RESULT 15
 A46474
 Fc epsilon RIIB - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
 C;Accession: A46474
 R;Richards, M.L.; Katz, D.H.; Liu, F.T.
 J. Immunol. 147, 1067-1074, 1991
 A;Title: Complete genomic sequence of the murine low affinity Fc receptor for IgE. Demonstration of a single gene for the Fc epsilon RIIB.
 A;Reference number: A46474; MUID:91318149
 A;Accession: A46474
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-6 <RIC>
 A;Experimental source: BALB C, splenic B cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:45428)

Query Match 28.9%; Score 13; DB 2; Length 6;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 vdls 6
 |||
 Db 1 MDTHH 5

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